Genome Sequence of *Corynebacterium nuruki* S6-4T, Isolated from Alcohol Fermentation Starter

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*Corynebacterium nuruki* S6-4T, isolated from Korean alcohol fermentation starter, is a strictly aerobic, nonmotile, Gram-positive, and rod-shaped bacterium belonging to the genus *Corynebacterium* and the actinomycete group. We report here the draft genome sequence of *C. nuruki* strain S6-4T (3,106,595 bp, with a G+C content of 69.5%).

The unclosed draft genome was 3,106,595 bp in length and had a G+C content of 69.5%. Two rRNA genes (5S-16S) and 56 tRNA genes in the draft assembly were identified by tRNAscan-SE 1.23 (5) and RNAmmer 1.2 (4), respectively. Open reading frames (ORFs) of large contigs were predicted by six-reading-frame translation (7) and annotated against the COG database (RPS-BLAST, E value of <10−7) (1) with the CAMERA server, version 2.0.6.3 (http://camera.calit2.net/). Consequently, 2,832 coding sequences (CDSs) and 109 subsystem features were predicted with 18 COG categories (J, K, L, D, V, T, M, U, O, C, G, E, F, H, P, Q, R, and S). It contains 10 predicted genes for amino acid transport and metabolism and 9 predicted genes for carbohydrate transport and metabolism. These results perhaps reflect the food-grade ecological niche of the organism presented in the alcohol fermentation starter for amylolytic machinery.

**Nucleotide sequence accession numbers.** The draft genome sequence of *Corynebacterium nuruki* strain S6-4T reported in this paper has been deposited in DDBJ/EMBL/GenBank under accession number AFIZ00000000 and in GenBank under Genome Project ID number 66913. The version described in this paper is the first version, accession number AFIZ01000000.

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**REFERENCES**